

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: September 27, 2001, 16:40:12 ; Search time 38.23 Seconds
 1100.523 Million cell updates/sec

Title: US-09-483-543A-8
 perfect score: 1693
 Sequence: 1 KRGCAGNFDSEERSSWWGR... QQNPDEDPSGCGXGLEVLFO 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPTREMBL_16:
 1: sp_archaea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_mhc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp_rabbit:
 12: sp_unclassified:
 13: sp_vertebrate:
 14: sp_virus:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT	1
ID	Q9W60
AC	Q9W60;
DT	01-MAY-2000 (TREMBLrel. 13, created)
DT	01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT	01-MAR-2001 (TREMBLrel. 15, last annotation update)
DE	GRB-3 EPIDERMAL GROWTH FACTOR-RECEPTOR-BINDING PROTEIN
OS	Mus sp.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murida; Murinae; Mus.
OX	NCBI_TaxID=10095;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE:93028373; PubMed=1409582;
RA	Margolis B., Silvennoinen O., Comoglio F., Rooprapunt C., Skolnik E., Ulrich A., Schlessinger J.;
RT	"High-efficiency expression/cloning of epidermal growth factor-receptor-binding proteins with SRC homology 2 domains.",
RT	Proc. Natl. Acad. Sci. U.S.A. 89:8894-8898(1992).
DR	DR InterPro: IPR00452; -.
DR	InterPro: IPR00452; -.
DR	InterPro: IPR00452; -.
DR	PFAM: PF00017; SH2; 1.
DR	PFAM: PF00018; SH3; 1.
DR	PRINTS: PR00401; SH2DOMAIN.
DR	PRINTS: PR00452; SH3DOMAIN.
DR	PROSITE: PS00001; SH2; 1.
DR	PROSITE: PS50002; SH3; 1.
DR	SMART: SM00326; SH3; 1.
DR	SEQUENCE 239 AA; 26013 MW; 48326D680C9F09B6 CRC64;

Query Match Best Local Similarity 63.7%; Score 1078; DB 11; Length 239; Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

19 1097 5 Q9U2T9

Result No.	Score	Query Match Length	DB ID	Description
1	1078	63.7	239	11 Q9OWK0
2	834.5	49.3	255	14 Q99059
3	343	20.3	279	5 Q9NHIC3
4	213	12.6	217	13 Q9PVU1
5	200	11.8	600	5 Q9VE96
6	193	11.4	1067	13 Q9YH06
7	184.5	10.9	1010	13 Q9YHU7
8	182	10.8	1097	5 Q9U2T9
9	173	10.2	640	4 Q9W593
10	173	10.2	666	4 Q9W592
11	170	10.0	816	4 Q9UF72
12	165	9.7	1270	13 Q42287
13	164	9.7	1196	11 Q35413
14	163.5	9.7	857	3 Q9P7E8
15	163	9.6	684	4 Q9Y338
16	162	9.6	815	4 Q9P2Q0
17	161	9.6	1217	11 Q9WVE9
18	161	9.5	1094	5 Q9W1F7
19	1097	5 Q9VIF7		

RESULT 2

Q99059 PRELIMINARY; PRT; 255 AA.

ID Q99059; PRELIMINARY;

AC 099059; PRELIMINARY;

DT 01-NOV-1996 (TREMBREL. 01, Created)

DT 01-NOV-1996 (TREMBREL. 01, Last sequence update)

DT 01-MAR-2001 (TREMBREL. 16, Last annotation update)

DE GAG-CRK PROTEIN (FRAGMENT).

OS Avian sarcoma virus 1.

OC Viruses; Retroviriidae; Avian type C retroviruses.

OX NCBI_TAXID=11957;

RN [1]

SEQUENCE FROM N.A.

MEDLINE=004469; PUBMED=2554234;

RA Tsuchie H., Chang C.H.W., Yoshida M., Vogt P.K.

RT "A newly isolated avian sarcoma virus, ASV-1, carries the crk oncogene.";

RL Oncogene 4:1281-1284 (1989).

CC -1- SIMILARITY: CONTAINS A COPY EACH OF THE SH2 AND SH3 DOMAINS.

DR EMBL; X1292; CAA35181.1; -.

DR HSSP; Q64010; ICKA;

DR InterPro; IPRO00980; -.

DR InterPro; IPRO01452; -.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3; 1.

DR PRINTS; PR00401; SH3DOMAIN.

DR PROSITE; PS50001; SH2; 1.

DR PROSITE; PS50002; SH3; 1.

DR SMART; SM0326; SH3; 1.

KW Oncogene; Polyprotein; SH3 domain; SH2 domain.

FT NON_TER 1 < 23 GAG (BY SIMILARITY).

FT DOMAIN 24 253 CRK (BY SIMILARITY);

FT DOMAIN 63 112 SH2 (OR B+C BOX) (BY SIMILARITY).

FT DOMAIN 188 239 SH3 (OR A BOX) (BY SIMILARITY).

FT DOMAIN 254 255 GAG (BY SIMILARITY).

SQ SEQUENCE 255 AA; 27985 MN; 0C562B02327A579 CRC64;

Query Match 20.3%; Score 343; DB 5; Length 279;

Best Local Similarity 31.0%; Pred. No. 9_9e-21;

Matches 93; Conservative 52; Mismatches 111; Indels 44; Gaps 9;

Matches 93; Conservative 52; Mismatches 111; Indels 44; Gaps 9;

QY 8 FDSEERSSWMWGRSLRQEAVALLOGQRH--GVFLVRDSSISPGDYVLSV--SENSRVS 61

DB 6 FDPFEWSFVFPGMSREERAHKL-GEPQVSGITFLMRS S-RPGEVSLTVRADEGNAVC 63

QY 62 HYITNSSGPRPPVPPSPAGPPPEVPSPLRURIGQEEFSPLALLEPFKHYDTTTLEPV 121

DB 111 -----RAYKKPTIEVVGTFKFTGERTEDLPFEGOERLILSKTNQDWEARNALGT 162

QY 182 RGMIVPVYEE--KYPASAVSVALIGGNGEKGSHPQPLGGPERGPQAQPSTNPMLNQ- 237

DB 64 HYLLERGERK-----EDGIAAKVKIANQSFPDPIALNHKMRVTEASIL-- 110

QY 122 ARSROGSGVILRQEAEYVRALEDFNGNEDELPKGDILIRKDPEEQWNAESEGK 181

DB 111 -----RAYKKPTIEVVGTFKFTGERTEDLPFEGOERLILSKTNQDWEARNALGT 162

QY 163 TGLIPVANYIQMFERHNDRTS-----KQASOSSGSGGAERFSSASTSSDNIEL 213

DB 238 --NGPTYARIQKRVNPAYDKTAALEGELEVKTINNSGOWEGECNGKRGHFPPTH 295

QY 238 --NGPTYARIQKRVNPAYDKTAALEGELEVKTINNSGOWEGECNGKRGHFPPTH 295

DB 214 QPRLEAKANVTFDRVPNAXDPTQIQRVKKGQTIVTQMSNGWKAELDGQITGSVPTYL 273

Query Match 49.3%; Score 834.5; DB 14; Length 255;

Best Local Similarity 78.3%; Pred. No. 1.5e-61;

Matches 159; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

RESULT 3

Q9NHC3 PRELIMINARY; PRT; 279 AA.

ID Q9NHC3; PRELIMINARY;

AC 09NHC3; PRELIMINARY;

DT 01-OCT-2000 (TREMBREL. 15, Created)

DT 01-OCT-2000 (TREMBREL. 15, Last sequence update)

DE CELL-CORSE ENGULFMENT PROBIN CED-2.

GN CED-2.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditida; Plecterinae; Caenorhabditis.

OX NCBI_TAXID=6239;

RN [1]

SEQUENCE FROM N.A.

RP Reddien P.W., Horvitz H.R.;

RT "CED-2/Crk1 and CED-10/Rac control phagocytosis and cell migration in C. elegans"; Nat. Cell Biol. 0:0-0(2000).

RT C. elegans; Nat. Cell Biol. 0:0-0(2000).

RL EMBL; AF226866; AAAF33845.1; -.

DR InterPro; IPRO00980; -.

DR InterPro; IPRO01452; -.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3; 2.

DR PRINTS; PR00401; SH2DOMAIN.

DR PRINTS; PR00422; SH3DOMAIN.

DR PROSITE; PS50001; SH2; 1.

DR PROSITE; PS50002; SH3; 1.

DR SEQUENCE 279 AA; 30878 MN; 5CE7DA478948970B CRC64;

Query Match 20.3%; Score 343; DB 5; Length 279;

Best Local Similarity 31.0%; Pred. No. 9_9e-21;

Matches 93; Conservative 52; Mismatches 111; Indels 44; Gaps 9;

Matches 93; Conservative 52; Mismatches 111; Indels 44; Gaps 9;

QY 8 FDSEERSSWMWGRSLRQEAVALLOGQRH--GVFLVRDSSISPGDYVLSV--SENSRVS 61

DB 6 FDPFEWSFVFPGMSREERAHKL-GEPQVSGITFLMRS S-RPGEVSLTVRADEGNAVC 63

QY 62 HYITNSSGPRPPVPPSPAGPPPEVPSPLRURIGQEEFSPLALLEPFKHYDTTTLEPV 121

DB 111 -----RAYKKPTIEVVGTFKFTGERTEDLPFEGOERLILSKTNQDWEARNALGT 162

QY 182 RGMIVPVYEE--KYPASAVSVALIGGNGEKGSHPQPLGGPERGPQAQPSTNPMLNQ- 237

DB 64 HYLLERGERK-----EDGIAAKVKIANQSFPDPIALNHKMRVTEASIL-- 110

QY 122 ARSROGSGVILRQEAEYVRALEDFNGNEDELPKGDILIRKDPEEQWNAESEGK 181

DB 111 -----RAYKKPTIEVVGTFKFTGERTEDLPFEGOERLILSKTNQDWEARNALGT 162

QY 163 TGLIPVANYIQMFERHNDRTS-----KQASOSSGSGGAERFSSASTSSDNIEL 213

DB 238 --NGPTYARIQKRVNPAYDKTAALEGELEVKTINNSGOWEGECNGKRGHFPPTH 295

QY 238 --NGPTYARIQKRVNPAYDKTAALEGELEVKTINNSGOWEGECNGKRGHFPPTH 295

DB 214 QPRLEAKANVTFDRVPNAXDPTQIQRVKKGQTIVTQMSNGWKAELDGQITGSVPTYL 273

RESULT 4

Q9PUI1 PRELIMINARY; PRT; 217 AA.

ID Q9PUI1; PRELIMINARY;

AC Q9PUI1; PRELIMINARY;

DT 01-MAY-2000 (TREMBREL. 13, Created)

DT 01-MAY-2000 (TREMBREL. 13, Last sequence update)

DT 01-MAR-2001 (TREMBREL. 16, Last annotation update)

DE GRB2 PROTEIN.

OS Xenopus laevis (African clawed frog).

OC Bokaiyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TAXID=8355;

RN [1]

SEQUENCE FROM N.A.

RP Goisset C., Shi D.L., Boucalt J.C.,

RT	"Selective inhibition of neural induction but not mesoderm induction by interfering mutants of Sem-5/Grb2."
RT	Submitted (DQC-1987) to the EMBL/GenBank/DBJ databases.
RL	HSSP; P29354; IGH0.
DR	InterPro; IPR000108; -.
DR	InterPro; IPR00080; -.
DR	InterPro; IPR001452; -.
DR	Pfam; PF00017; SH2; 1.
DR	Pfam; PF00018; SH3; 2.
DR	PRINTS; PR00499; P67PHOX.
DR	PRINTS; PR00452; SH3DOMAIN.
DR	PROSITE; PS50001; SH2; 1.
DR	PROSITE; PS50002; SH3; 2.
DR	SMART; SM00326; SH3; 1.
SQ	SEQUENCE 217 AA; 25135 MW; 2349A68260F9D4CD CRC64;
Query	Match 12.6%; Score 213; DB 13; Length 217;
Best	Local Similarity 27.4%; Pred. No. 4.3e-10;
Matches	52; Conservative 45; Mismatches 57; Indels 36; Gaps 7;
QY	7 NFDSEERSSWYWGRSLRSROBAVALLIQGQRH-GVFLVRSSTSRSQDVYVSSEMNSRVSHTI 65
Db	51 NYIEMKAHWPWFEGKIPRAKAEEMLGKQRHDGAFLIRESESARCFDSLSVKFGNDVQHFKV 110
QY	66 NSSSPRPVPPSPQPPGPGVSPSRURGQDQEFSQSPALLEFYKHYLDTTLIEPVARS 125
Db	111 LRDG-----AGGYFLAWVKFNLSNLNEDVH-----STS-----VERNO 144
QY	126 QGSQVILRQ----EEAEVRALEDFNGNDEEDLPFKKGDLIRIRDKEEQMANEDSEG 180
Db	145 Q---IFLRDIEQVHQOPTVVOALFDFDPOEQDGEGLGERGDFIQWVDNSDPNWAKG-TCLS 200
QY	181 KRGMTPVYYV 190
Db	201 QTGMFPRNTV 210
RESULT	5
Q9VE96	PRELIMINARY; PRT; 600 AA.
AC	Q9VE96
DT	01-MAY-2000 (TREMBREL. 13, Created)
DT	01-MAY-2000 (TREMBREL. 13, Last sequence update)
DT	01-MAR-2001 (TREMBREL. 16, Last annotation update)
DE	CG7129 PROTEIN.
GN	CG7129.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydriidae; Drosophilidae; Drosophila.
NCBI_TAXID	7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BERKELEY;
RX	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hostkins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandt R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Prefffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G., Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Batzakaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S., Borkstein P., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahake C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dev I., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunker B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RESULT	6
Q9HU6	PRELIMINARY; PRT; 1067 AA.
ID	Q9HU6
AC	Q9HU6;
DT	01-MAY-1999 (TREMBREL. 10, Created)
DT	01-MAY-1999 (TREMBREL. 10, Last sequence update)
DT	01-MAR-2001 (TREMBREL. 16, Last annotation update)
DE	PHOSPHOLIPASE C GAMMA-1B (FRAGMENT).
OS	Xenopus laevis (African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kung H.-F., Kim J., Huang Y.K., Lin M.C.;
 RT "Molecular cloning of two different forms of *Xenopus* phospholipase C-
 gamma-1", Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF090112; AAD03595.1; -.
 DR HSSP; P08487; 2PLD;
 DR InterPro; IPR000008; -.
 DR InterPro; IPR000909; -.
 DR InterPro; IPR000980; -.
 DR InterPro; IPR001192; -.
 DR InterPro; IPR001452; -.
 DR InterPro; IPR001711; -.
 DR InterPro; IPR001849; -.
 DR InterPro; IPR002048; -.
 DR Pfam; PF00017; SH2; 2.
 DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00169; PH; 2.
 DR Pfam; PF00387; PI_PLC_Y; 1.
 DR Pfam; PF00388; PI_PLC_X; 1.
 DR Prints; PR00390; PIPLIPASEC.
 DR Prints; PR00401; SH2DOMAIN.
 DR Prints; PR00452; SH3DOMAIN.
 DR PROSITE; PS0004; C2_DOMAIN; 2; 1.
 DR PROSITE; PS0018; EF_HAND; UNKNOWN_1.
 DR PROSITE; PS5003; PH_DOMAIN; 1.
 DR PROSITE; PS5008; PIPLC_Y_DOMAIN; 1.
 DR PROSITE; PS5001; SH2; 2.
 DR PROSITE; PS5002; SH3; 1.
 DR SMART; SM0239; C2; 1.
 FT NON_TER 1067 1067
 FT SEQUENCE 1067 AA; 124019 MW; 533F6876BCDFE5DB CRC64;
 SQ
 Query Match 11.4%; Score 193; DB 13; Length 1067;
 Best Local Similarity 21.7%; Pred No. 1.6e-07;
 Matches 95; Conservative 43; Mismatches 123; Indels 176; Gaps 17;
 QY 3 GCAGNFDSER------SSWYGRLL-----SRQEAVALL-----QGQRIGVFL 39
 Db 396 GSQANDDEEEBQEAKNEASNSSEBLHSAEKWFHGKLGAGRDRHIAERLLTDYCINGAPDSFL 455
 QY 40 VRDSTSPPGDYVLSSENSRSHYIINS--SGPR-----71
 Db 456 VRESETFVGDYTSFWRKVQHCRIHSROEAQSPKLLTDLNUFLVFSYLALITHYQOMPL 515
 QY 72 -----PPVPPPSAQ-----PPPGVSPSLR-----91
 Db 516 RCNEFEMRLTEPVQFQTNHESKEWKWHASLRLRGQAEMHLMRVFRDGAFLVRKRSEQNSYAI 575
 QY 92 -----IGDQEFDSLPALEFY-----KHYLDTTILEPV 121
 Db 576 SFRAEKGKIKHRCVIQEGOSVWLGSSEFDLSVLVDLISYEHKPMKMKLRPINETLEKI 635
 QY 122 ARSROSGSGYILRQEAEY-----VALFFNGNDEEDLFKKGDLRLTRDKP 168
 Db 636 GTPDPDYGALYEGRNPGFTVEANMPMFTKCSVRLFDYKAQREDELIFTKNTIONVEQ 695
 QY 169 EEEQWNAEDESEGKGM-TPVWYK-YRPA-----SASVSALEG-----71
 Db 696 EGWWWRG-DCCGKIKQMWFNPANYVEIFSPAEPERPERONLDENSPLGDLIGGVLDVPSCHI 754
 QY 207 --NOEGSHQP---LGGPEPGVYQPSVNTPIPNLQNGPIAVRVIOKRVPA-----253
 Db 755 APRODVHNGRPVFTTGPOLNQYPLDVAAADTLEMD--WIRKTIREAQTADARLTERG 811
 QY 254 --YKTALEALEYELV 267
 SQ
 Query Match 10.9%; Score 184.5; DB 13; Length 1010;
 Best Local Similarity 22.5%; Pred No. 7.6e-07;
 Matches 84; Conservative 28; Mismatches 101; Indels 161; Gaps 14;
 QY 3 GCAGNFDSER------SSWYGRLL-----SRQEAVALL-----QGQRIGVFL 39
 Db 318 GSQANDDEEEBQEAKNEASNSSEBLHSAEKWFHGKLGAGRDRHIAERLLTDYCINGAPDSFL 377
 QY 40 VRDSTSPPGDYVLSSENSRSHYIINS--SGPR-----71
 Db 378 VRESETFVGDYTSFWRKVQHCRIHSROEAQSPKLLTDLNUFLVFSYLALITHYQOMPL 437
 QY 72 -----PPVPPPSAQ-----PPPGVSPSLR-----91
 Db 438 RCNEFEMRLTEPVQFQTNHESKEWKWHASLRLRGQAEMHLMRVFRDGAFLVRKRSEQNSYAI 497
 QY 92 -----IGDQEFDSLPALEFY-----KHYLDTTILEPV 121
 Db 498 SFRAEKGKIKHRCVIQEGOSVWLGSSEFDLSVLVDLISYEHKPMKMKLRPINETLEKI 557

QY	122 ARSRQGSGVILRQEAEY-----VRALEDFNGNDEEDLFKKGDILRKDKE 168
Db	558 GTPPDYGYALYERGNPGFYVEAMPMPFKCSYRALKAGREDELTEFRNTLTONVEKO 617
QY	169 EEDQWNAEDESEGRGM LPVPMVEK YRPASASVSALLGGNQEGSHPQPLGGPERGPYAO 226
Db	618 EGSMWRC-DGGKQMFPAINTMEEIFSP-----PRPEPERQ 653
QY	227 P-SVNTPLNPLONG 239
Db	654 HLDBNSPLGLLG 667
RESULT	8
Q9UZT9	PRELIMINARY; PRT; 1097 AA.
ID	Q9UZT9
AC	Q9UZT9;
DT	01-MAY-2000 (TREMBlrel. 13, Created)
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT	01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE	Y116A8C 36 PROTEIN.
GN	Y116A8C 36.
OS	Caenorhabditis elegans.
OC	Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderrinae; Caenorhabditis.
OC	NCBI_TaxID=6239;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Mcmurray A.A.;
RL	Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.; PubMed=9851916;
RX	MEDLINE-99069613;
RA	none;
RT	"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology.";
RT	Science 282(5202):2018 (1998).
CC	-!!- SIMILARITY: TO EF HAND FAMILY.
DR	EMBL; ALI1204; CRB55138.1; -.
DR	HSSP; P29355; ISEM.
DR	InterPro; IPR000108; -.
DR	InterPro; IPR000194; -.
DR	InterPro; IPR00241; -.
DR	InterPro; IPR00142; -.
DR	InterPro; IPR002048; -.
DR	Pfam; PF00016; SH1; 5.
DR	Pfam; PF00036; effhand; 2.
DR	PRINTS; PR00499; p67PHOX.
DR	PRINTS; PR00452; SH3DOMAIN.
DR	PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
DR	PROSITE; PS00018; EF_HAND; UNKNOWN_2.
DR	PROSITE; PS50002; SH3; 5.
DR	SMART; SM00054; EH1; 1.
KW	Calcium-binding.
SQ	SEQUENCE 1097 AA: 122071 MW: 1C2BA5F103968372 CRC64:
Query Match	10.8%; Score 182; DB 5; Length 1097;
Best Local Similarity	21.2%; Pred. No. 1.4e-06;
Matches	75; Conservative 56; Mismatches 144; Indels 78; Gaps 14;
QY	6 GNFPSSEENNSWW---WGSLSRQEAVALLQSORH-----GVFLVRRD----- 43
Db	627 GEFDKTDASQRFADFGATSTADPFQIAQAPAHSKGAVDOSAFNIDTYKCRALFAEA 686
QY	44 -----SPSPGDVVLVSESENS-----RVSH-----LNSSGRPPVPP 76
Db	687 RSEDELSTFPGDVLLIVFOSHAREPGWRAGQLRKEVKGWPFPFVEATAVAPIPGSDPPIQ 746
QY	77 SPAGGPPPGVSPSPSLRIGQDEFELSPALLEYFVHYIHDFTTLIEPVARSRGSGVILRQE 135
Db	747 MPNPMTPSSVSDQIGVKARKAETAA-----MGLTEGGAPPASSAAPAAVISOCI 798
RESULT	9
Q9UZT9	PRELIMINARY; PRT; 640 AA.
ID	Q9UZT9
AC	Q9UZT9;
DT	01-AUG-1998 (TREMBlrel. 07, Created)
DT	01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT	01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE	ARG/ABL-INTERACTING PROTEIN ARGPBP2 (FRAGMENT).
GN	ARGBP2B.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Wang B., Golemis E.A., Kruth G.D.;
RT	Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
RT	"ArgBP2, a multiple src homology 3 domain-containing Arg(Abl)-interacting protein, is phosphorylated in v-Abl-transformed cells and localized in stress fibers and cardiotrocyte Z-disks.";
RL	J. Biol. Chem. 272:17542-17550(1997).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Wang B., Golemis E.A., Kruth G.D.;
RT	Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF049885; AAC05509.1; -.
DR	HSSP; P29354; IGRIT.
DR	InterPro; IPR00108; -.
DR	InterPro; IPR00452; -.
DR	InterPro; IPR00265; -.
DR	InterPro; IPR003127; -.
DR	Pfam; PF00018; SH1; 2.
DR	Pfam; PF02208; Sorb; 1.
DR	PRINTS; PR00499; p67PHOX.
DR	PRINTS; PR00217; PRICHEXTNSN.
DR	PRINTS; PR00452; SH3DOMAIN.
DR	PROSITE; PS50002; SH3; 2.
DR	SMART; SM00326; SH3; 1.
DR	SMART; SM00326; SH3; 2.
FT	NON_TER 640 AA: 70660 MW: 030A8C5036331674 CRC64;
SQ	SEQUENCE 640 AA: 70660 MW: 030A8C5036331674 CRC64:
Query Match	10.2%; Score 173; DB 4; Length 640;
Best Local Similarity	26.0%; Pred. No. 3.7e-06;
Matches	72; Conservative 29; Mismatches 92; Indels 84; Gaps 12;
QY	43 SSSSPGDPYLVLSSENSRVSHVHTINSSGPRPPPPSAQPP-----PGVSPSLRIG 93
Db	393 SRTSPGVDLPGSSTTLKSP--TSSSPSSPRAKDRDREPSRSYSTLDMGRSPRERRG 450
QY	94 DQFDSLPALEFYKIHLDITLIEPVARSQSGVILRQEAEYVRALFDNGNDEED 153
Db	451 TPEKEUPA-----KAVYDFKAPEA 472
QY	154 LPRKKGDILRKPKRQEWQWADSEGKRMIPVYVKRASASVALLGGNQEGSHP 213
Db	473 LSKKGDIVYTKRQDNWYGE-HIGRVGFLPEISYVEKIP----- 513
QY	214 QPLGGPERGPYQPSVNTPLNLONGPIVARYTORVNPAYDKTALALEGVLYVKIN 273

RESULT	10		
60592		PRELIMINARY;	PRT; 666 AA.
ID	060592;		
AC			
DT	01-AUG-1998 (TREMBLrel. 07, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DE	ARG/ABL-INTERACTING PROTEIN ARGP2A.		
GN	ARGP2A.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Butheroidea; Primates; Catarrhini; Hominidae; Homo.		
OX			
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=BRAIN;		
RX	MEDLINE=97362243; PubMed=9211900;		
RA	Wang B., Golemis E.A., Kruh G.D.,		
RA	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
RA	Mammalia; Butheroidea; Primates; Catarrhini; Hominidae; Homo.		
RT	"ArgP2, a multiple src homology 3 domain-containing, Arg/abl-interacting protein, is phosphorylated in v-Ab1-transformed cells and localized in stress fibers and cardiacocyte Z-disks.";		
RT	J. Biol. Chem. 272:17542-17550(1997).		
RL	(2)		
RN	SEQUENCE FROM N.A.		
RC	TISSUE=BRAIN;		
RX	Wang B., Golemis E.A., Kruh G.D.,		
RX	Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.		
RL	EMBL; AF049884; AAC05508.1; .		
DR	HSSP; P29554; IgR1.		
DR	InterPro; IPR001452; .		
DR	InterPro; IPR003127; .		
DR	Pfam; PF00018; SH3; 3.		
DR	Pfam; PF02208; Sorb; 1.		
DR	PRINTS; P001658; SH3DOMAIN.		
DR	PRINTS; P001658; SH3DOMAIN.		
DR	PROSITE; PS50002; SH3; 3.		
DR	SMART; SM0326; SH3; 1.		
DR	SMART; SM0326; SH3; 1.		
SQ	SEQUENCE 666 AA; 74803 MW; B549A26DC04782E0 CRC64;		
Query	Match	10.0%; Score 170; DB 4;	Length 816;
Best	Local Similarity	25.1%; Pred. No. 9.1e-06;	
Matches	69;	Conservative 34; Mismatches 100;	
		Indels 72; Gaps 12;	
QY	43	SSTSPEDYIVLSVENSRSRVSHWIINSSGRPPVPPSPAQPP-----FGVSPSLRIG 93	
Db	501	RESDAGPD--LTSLENEROIYKSYLEGSDIPQGLSGKURSSASTKDSBSPR----- 553	
QY	94	DOEFDSPALLEFYKHYLDPTTLEPVARSROSGGVILRQEAEYRALDFNGNDEED 153	
Db	554	-----HEIPADYLEST--EEFRRRHD---DKEMRPARAKDFKAOTIKE 593	
QY	154	LFFKGDLRLTRDKPKPEQWNNAEDSEKGKGMIPVYPERYKRRPASASVYSLIGGNQEGSHP 213	
Db	594	LPLQKGDIVVYKQLDQNWYEGE-HHGRYGFPIPYTIELLPKEK----- 637	
QY	214	QPLGGPFPYQKPSNTPLPNLQNGPITKAVIKRKNAYDKTALALEVGELVKYTKIN 273	
Db	638	-----AQPKLTPVQYVLE---YGEAIKAFNNGDITOVEMSFRGERITLR-Q 681	
QY	274	VSGQW-EGCNG-KRGHFFTHVLLDQ--QNP 302	
Db	682	VDENWYEGKPGTTSRQGIFTYVYDVKPLVKNP 716	
RESULT	12		
ID	042287	PRELIMINARY;	PRT; 1270 AA.
AC	042287;		
DT	01-JAN-1998 (TREMBLrel. 05, Created)		
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)		
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DE	INTERSECTIN		
DE	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;		
OC	Xenopoda; Xenopus.		
OX	NCBI_TaxID=8355;		
PN	[1]		

